

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Oon, Chong Jin

Lim, Gek Keow

Zhao, Yi

Chen, Wei Ning

(ii) TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

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(D) STATE: New York

(E) COUNTRY: USA

(F) ZIP: 10023

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/719,528

(B) FILING DATE: 19-DEC-2000

(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/SG98/00046

(B) FILING DATE: 19-JAN-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mass, Clifford J.

(B) REGISTRATION NUMBER: 30,086

(C) REFERENCE/DOCKET NUMBER: U-014987-0

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 708-1800

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCCACAACA TTCCACCAAG CTCTGCTAGA TCCCAGGGTG AGGGGCCTAT
ATTTTCCTGC 60

TGGTGGCTCC AGTTCCGGAA CAGTAAACCC TGTTCCGACT ACTGCCTCTC
CCATATCGTC 120

AATCTTCTCG AGGACTGGGG ACCCTGCACC GAACATGGAG AACACAACAT
CAGGATTCCT 180

AGGACCCCTG CTCGTGTTAC AGGCGGGGTT TTTCTCGTTG ACAAGAATCC
TCACAATACC 240

GCAGAGTCTA GACTCTGGTG GACTTCTCTC AATTTTCTAG GGGGAGCACC
CACGTGTTCC 300

TGGCCAAAAT TCGCAGTCCC CAACCTCCAA TCACTCACCA ACCTCTTGTC
CTCCAATTTG 360

TCCTGGCTAT CGCTGGATGT GTCTGCGGCG TTTTATCATA TTCCTCTTCA
TCCTGCTGCT 420

ATGCCTCATC TTCTTGTTGG TTCTTCTGGA CTACCAAGGT ATGTTGCCCG
TTTGTCTCT 480

ACTTCCAGGA ACATCAACCA CCAGCACGGG GCCATGCAAG ACCTGCACGA
CTCCTGCTCA 540

AGGAAACTCT ACGTTTCCCT CTTGTTGCTG TACAAAACCT TCGGACGGAA
ACTGCACTTG 600

TATTCCCATC CCATCATCCT GGGCTTTCGC AAGATTCCTA TGGGAGTGGG
CCTCAGTCCG 660

TTTCTCCTGG CTCAGTTTAC TAGTGCCATT TG TTCAGTGG TTCGTAGGGC
TTTCCCCCAC 720

TGTTTGGCTT TCAGTTATAT GGATGATGTG GTATTGGGGG CGAAGTCTGT
ACAACATCTT 780

GAGTCCCTTT TTACCTCTAT TACCAATTTT CTTTGTCTT TGGGTATACA
TTTAAACCCT 840

AATAAAACCA AACGTTGGGG CTA CTCCCTT AACTTCATGG GATATGTAAT
TGGAAGTTGG 900

GGTACTTTAC CGCAGGAACA TATTGTACTA AA ACTCAAGC AATGTTTTCG
AAA ACTGCCT 960

GTAAATAGAC CTATTGATTG GAAAGTATGT CAAAGAATTG TGGGTCTTTT
GGGCTTTGCT 1020

GCCCCTTTTA CACAATGTGG CTATCCTGCC TTGATGCCTT TATATGCATG
TATACAATCT 1080

AAGCAGGCTT TACTTTCTC GCCAACTTAC AAGGCCTTTC TGTGTAAACA
ATATCTGAAC 1140

CTTTACCCCG TTGCCCGGCA ACGGTCCGGT CTCTGCCAAG TGTTTGCTGA
CGCAACCCCC 1200

ACTGGATGGG GCTTGGCCAT AGGCCATCAG CGCATGGCTG GAACCTTTCT
GGCTCCTCTG 1260

CCGATCCATA CTGCGGAACT CCTAGCAGCT TGTTTTGCTC GCAGCCGGTC
TGGAGCAAAA 1320

CTTATCGGAA CCGACAACTC TGTTGTCCTC TCTCGGAAAT ACACCTCCTT
TCCATGGCTG 1380

CTAGGGTGTG CTGCCAACTG GATCCTGCGC GGGACGTCCT TTGTCTACGT
CCCGTCGGCG 1440

CTGAATCCCG CGGACGACCC GTCTCGGGGC CGTTTGGGGC TCTACCGTCC
CCTTCTTCAT 1500

CTGCCGTTCC GGCCGACCAC GGGGCGCACC TCTCTTTACG CGGTCTCCCC
GTATGTGCCT 1560

TCTCATCTGC CGGACCGTGT GCACTTCGCT TCACCTCTGC ACGTCGCATG
GAGACCACCG 1620

TGAACGCACG CCAGGTCTTG CCCAAGGTCT TATATAAGAG GACTCTTGGA
CTCTCAGCAA 1680

TGTCAACGAC CGACCTTGAG GCATACTTCA AAGACTGTGT GTTTAAAGAC
TGGGAGGAGT 1740

TGGGGGAGGA GATTAGGTTA AAGATTTATG TACTAGGAGG CTGTAGGCAT
AAATTGGTCT 1800

G TTCACCAGC ACCATGCAAC TTTTCTCCT CTGCCTAATC ATCTCATGTT
CATGTCCTAC 1860

TGTTCAAGCC TCCAAGCTGT GCCTTGGGTG GCTTTGGGAC ATGGACATTG
ACCCGTATAA 1920

AGAATTTGGA GCATCTGCTG AGTTACTCTC TTTTTTGCCT TCTGACTTCT
TTCCGTCTAT 1980

TCGAGATCTC CTCGACACCG CCTCTGCTCT GTATCGGGAG GCCTTAGAGT
CTCCGGAACA 2040

TTGTTGCGCT CACCATACAG CACTCAGGCA AGCTATTTTG TGTTGGGGTG
AGTTGATGAA 2100

TCTGGCCACC TGGGTGGGAA GTAATTTGGA AGATCCAGCA TCCAGGGAAT
TAGTAGTCAG 2160

CTATGTCAAC GTTAATATGG GCCTAAAAC T CAGACAAATA TTGTGGTTTC
ACATTTCTG 2220

TCTTACTTTT GGAAGAGAAA CTGTTCTTGA GTACTTGGTA TCTTTTGGAG
TGTGGATTCTG 2280

CACTCCTACC GCTTACAGAC CACCAAATGC CCCTATCTTA TCAACACTTC
CGGAAACTAC 2340

TGTTGTTAGA CGACGAGGCA GGTCCCCTAG AAGAAGAACT CCCTCGCCTC
GCAGACGAAG 2400

GTCTCAATCG CCGCGTCGCA GAAGATCTCA ATCTCGGGAA TCTCAACGTT
AGTATTCCTT 2460

GGACTCATAA GGTGGGAAAC TTTACTGGGC TTTATTCTTC TACTGTACCT
GTCTTTAATC 2520

CCGAGTGGCA AATTCCTTCC TTTCTCACA TTCATTTACA AGAGGACATT
ATTAATAGAT 2580

GTCAACAATA TGTGGGCCCT CTTACAGTTA ATGAAAAAAG AAGATTAAAA
TTAATTATGC 2640

CTGCTAGGTT TTATCCTAAC CTTACTAAAT ATTTGCCCTT AGACAAAGGC
ATTAAACCGT 2700

ATTATCCTGA ACATGCAGTT AATCATTACT TCAAAACTAG GCATTATTTA
CATACTCTGT 2760

GGAAGGCTGG CATTCTATAT AAGAGAGAAA CTACACGCAG CGCCTCATTT
TGTGGGTCAC 2820

CATATTCTTG GGAACAAGAG CTACAGCATG GGAGGTTGGT CTTCCAAACC
TCGACAAGGC 2880

ATGGGGAGCA ATCTTGCTGT TCCAATCCT CTGGGATTCT TTCCCGATCA
CCAGTTGGAC 2940

CCTGCGTTCG GAGCCAATC AAACAATCCA GATTGGGACT TCAACCCCAA
CAAGGATCAC 3000

TGGCCAGAGG CAAATCAGGT AGGAGTGGGA GCATTCGGGC CAGGGTTCAC
CCCACCACAC 3060

GGCGGTCTTT TGGGGGGGAG CCCTCAGGCT CAGGGCATAT TGACAACAGT
GCCAGCAGCA 3120

CCTCCTCCTG CCTCCACCAA TCGGCAGTCA GGAAGACAGC CTA TCTCCCAT
CTCTCCACCT 3180

CTAAGAGACA GTCATCCTCA GGCCACGCAG TGGAA 3215

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 843 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
1 5 10 15

Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Gly
 20 25 30

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
 35 40 45

Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser
 50 55 60

Ser Thr Val Pro Val Phe Asn Pro Glu Trp Gln Ile Pro Ser Phe Pro
65 70 75 80

His Ile His Leu Gln Glu Asp Ile Ile Asn Arg Cys Gln Gln Tyr Val
 85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys Leu Ile Met Pro
 100 105 110

Ala Arg Phe Tyr Pro Asn Leu Thr Lys Tyr Leu Pro Leu Asp Lys Gly
 115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Ala Val Asn His Tyr Phe Lys Thr
 130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Thr Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
 165 170 175

Gln Glu Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Thr Arg His
 180 185 190

Gly Asp Glu Ser Cys Cys Ser Gln Ser Ser Gly Ile Leu Ser Arg Ser

195	200	205			
Pro Val Gly	Pro Cys Val Arg	Ser Gln Leu Lys	Gln Ser Arg	Leu Gly	
210	215	220			
Leu Gln Pro	Gln Gln Gly	Ser Leu Ala Arg	Gly Lys Ser	Gly Arg Ser	
225	230	235	240		
Gly Ser Ile	Arg Ala Arg	Val His Pro	Thr Thr Arg	Arg Ser Phe	Gly
245	250	255			
Gly Glu Pro	Ser Gly Ser	Gly His Ile	Asp Asn Ser	Ala Ser Ser	Thr
260	265	270			
Ser Ser Cys	Leu His Gln	Ser Ala Val Arg	Lys Thr Ala	Tyr Ser His	
275	280	285			
Leu Ser Thr	Ser Lys Arg	Gln Ser Ser	Ser Gly His	Ala Val Glu	Leu
290	295	300			
His Asn Ile	Pro Pro Ser	Ser Ala Arg	Ser Gln Gly	Glu Gly Pro	Ile
305	310	315	320		
Phe Ser Cys	Trp Trp Leu	Gln Phe Arg	Asn Ser Lys	Pro Cys Ser	Asp
325	330	335			
Tyr Cys Leu	Ser His Ile	Val Asn Leu	Leu Glu Asp	Trp Gly Pro	Cys
340	345	350			
Thr Glu His	Gly Glu His	Asn Ile Arg	Ile Pro Arg	Thr Pro Ala	Arg
355	360	365			
Val Thr Gly	Gly Val Phe	Leu Val Asp	Lys Asn Pro	His Asn Thr	Ala
370	375	380			
Glu Ser Arg	Leu Trp Trp	Thr Ser Leu	Asn Phe Leu	Gly Gly Ala	Pro
385	390	395	400		
Thr Cys Ser	Trp Pro Lys	Phe Ala Val	Pro Asn Leu	Gln Ser Leu	Thr
405	410	415			
Asn Leu Leu	Ser Ser Asn	Leu Ser Trp	Leu Ser Leu	Asp Val Ser	Ala
420	425	430			
Ala Phe Tyr	His Ile Pro	Leu His Pro	Ala Ala Met	Pro His Leu	Leu

435	440	445			
Val Gly Ser Ser Gly Leu Pro Arg Tyr Val Ala Arg Leu Ser Ser Thr					
450	455	460			
Ser Arg Asn Ile Asn His Gln His Gly Ala Met Gln Asp Leu His Asp					
465	470	475	480		
Ser Cys Ser Arg Lys Leu Tyr Val Ser Leu Leu Leu Tyr Lys Thr					
485	490	495			
Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe					
500	505	510			
Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln					
515	520	525			
Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys					
530	535	540			
Leu Ala Phe Ser Tyr Met Asp Asp Val Val Leu Gly Ala Lys Ser Val					
545	550	555	560		
Gln His Leu Glu Ser Leu Phe Thr Ser Ile Thr Asn Phe Leu Leu Ser					
565	570	575			
Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser					
580	585	590			
Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln					
595	600	605			
Glu His Ile Val Leu Lys Leu Lys Gln Cys Phe Arg Lys Leu Pro Val					
610	615	620			
Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu					
625	630	635	640		
Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro					
645	650	655			
Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr					
660	665	670			

Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala
675 680 685

Arg Gln Arg Ser Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr
690 695 700

Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Ala Gly Thr Phe Leu
705 710 715 720

Ala Pro Leu Pro Ile His Thr Ala Glu Leu Leu Ala Ala Cys Phe Ala
725 730 735

Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val
740 745 750

Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala
755 760 765

Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu
770 775 780

Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro
785 790 795 800

Leu Leu His Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr
805 810 815

Ala Val Ser Pro Tyr Val Pro Ser His Leu Pro Asp Arg Val His Phe
820 825 830

Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
835 840

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
1 5 10 15

Ala Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp His Trp Pro Glu Ala Asn Gln Val Gly Val Gly Ala Phe Gly
50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Gly Ser Pro Gln
65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser
85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
100 105 110

Arg Asp Ser His Pro Gln Ala Thr Gln Trp Asn Ser Thr Thr Phe His
115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro
145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
165 170 175

Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
180 185 190

Phe Phe Ser Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro

225	230	235	240
Pro Ile Cys Pro Gly Tyr Arg Trp Asn Cys Leu Arg Arg Phe Ile Ile			
	245	250	255
Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu			
	260	265	270
Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser			
	275	280	285
Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Thr Pro Ala Gln Gly			
	290	295	300
Asn Ser Thr Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn			
305	310	315	320
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu			
	325	330	335
Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro			
	340	345	350
Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val			
	355	360	365
Ile Trp Met Met Trp Tyr Trp Gly Arg Ser Leu Tyr Asn Ile Leu Ser			
	370	375	380
Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile			
385	390	395	400

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gln Leu Phe Leu Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
 20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Ser Ala Glu Leu Leu Ser Phe Leu
 35 40 45

Pro Ser Asp Phe Phe Pro Ser Ile Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Asn
 85 90 95

Leu Ala Thr Trp Val Gly Ser Asn Leu Glu Asp Pro Ala Ser Arg Glu
 100 105 110

Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys Leu Arg Gln
 115 120 125

Ile Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140

Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Thr Ala
 145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205

Glu Ser Gln Arg
 210

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Ala Arg Val Cys Cys Gln Leu Asp Pro Ala Arg Asp Val Leu
1 5 10 15

Cys Leu Arg Pro Val Gly Ala Glu Ser Arg Gly Arg Pro Val Ser Gly
20 25 30

Pro Phe Gly Ala Leu Pro Ser Pro Ser Ser Ala Val Pro Ala Asp
35 40 45

His Gly Ala His Leu Ser Leu Arg Gly Leu Pro Val Cys Ala Phe Ser
50 55 60

Ser Ala Gly Pro Cys Ala Leu Arg Phe Thr Ser Ala Arg Arg Met Glu
65 70 75 80

Thr Thr Val Asn Ala Arg Gln Val Leu Pro Lys Val Leu Tyr Lys Arg
85 90 95

Thr Leu Gly Leu Ser Ala Met Ser Thr Thr Asp Leu Glu Ala Tyr Phe
100 105 110

Lys Asp Cys Val Phe Lys Asp Trp Glu Glu Leu Gly Glu Glu Ile Arg
115 120 125

Leu Lys Ile Tyr Val Leu Gly Gly Cys Arg His Lys Leu Val Cys Ser
130 135 140

Pro Ala Pro Cys Asn Phe Phe Ser Ser Ala
145 150

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAAGCTTAT GCCCCTATCT TATCAACACT TCCGGA

36

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGTCTAGAC TCTGCGGTAT TGTGA

25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCTAGAC TCGTGGTGA CTTCT

25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGAATTCT CACGGTGGTC TCCATGCGAC GT

32

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGTTTACG TCCCGT

16

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAAGCTTAT GCCCCTATCT TATCAACACT TCCGGA

36